RAW SEQUENCE LISTING
ERROR REPORT

/16⟩² B.⊔.ʁECHNOLOGY
SYSTEMS-
BRANCH

165²
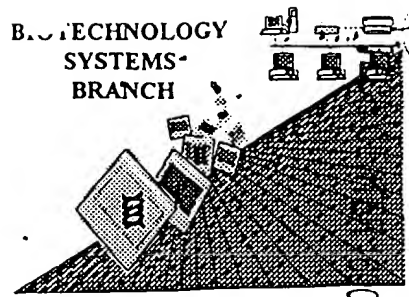
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___0 9/5 34 229 A___

Source: ___AU 1600___

Date Processed by STIC: ___11/14/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

1600

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/534,229A   TIME: 08:54:23

Input Set : A:\es.txt
Output Set: N:\CRF3\11142001\I534229A.raw

```
 3 <110> APPLICANT: Kawakami, Akira
 4         Terami, Fumihiro
 6 <120> TITLE OF INVENTION: LOW TERPERATURE EXPRESSION CHITINASE cDNAs AND METHOD FOR
ISOLATING THE
 7         SAME
 9 <130> FILE REFERENCE: 107156-00004
11 <140> CURRENT APPLICATION NUMBER: US 09/534,229A
12 <141> CURRENT FILING DATE: 2000-03-24
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 256
20 <212> TYPE: PRT
21 <213> ORGANISM: Triticum aestivum
23 <400> SEQUENCE: 1
25 Met Ala Arg Phe Ala Ala Leu Ala Val Cys Ala Ala Ala Leu Leu Leu
26 1               5                   10                  15
28 Ala Val Ala Ala Gly Gly Ala Ala Ala Gln Gly Val Gly Ser Val Ile
29             20                  25                  30
31 Thr Arg Ser Val Tyr Ala Ser Met Leu Pro Asn Arg Asp Asn Ser Leu
32         35                  40                  45
34 Cys Pro Ala Arg Gly Phe Tyr Thr Tyr Asp Ala Phe Ile Ala Ala Ala
35      50                  55                  60
37 Asn Thr Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Asp Ile Lys
38 65                  70                  75                  80
40 Arg Asp Leu Ala Ala Phe Phe Gly Gln Thr Ser His Glu Thr Thr Gly
41             85                  90                  95
43 Gly Thr Arg Gly Ala Ala Asp Gln Phe Gln Trp Gly Tyr Cys Phe Lys
44             100                 105                 110
46 Glu Glu Ile Ser Lys Ala Thr Ser Pro Pro Tyr Tyr Gly Arg Gly Pro
47         115                 120                 125
49 Ile Gln Leu Thr Gly Arg Ser Asn Tyr Asp Leu Ala Gly Arg Ala Ile
50      130                 135                 140
52 Gly Lys Asp Leu Val Ser Asn Pro Asp Leu Val Ser Thr Asp Ala Val
53 145                 150                 155                 160
55 Val Ser Phe Arg Thr Ala Met Trp Phe Trp Met Thr Ala Gln Gly Asn
56             165                 170                 175
58 Lys Pro Ser Cys His Asn Val Ala Leu Arg Arg Trp Thr Pro Thr Ala
59             180                 185                 190
61 Ala Asp Thr Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn
62         195                 200                 205
64 Ile Ile Asn Gly Gly Leu Glu Cys Gly Met Gly Arg Asn Asp Ala Asn
65      210                 215                 220
67 Val Asp Arg Ile Gly Tyr Tyr Thr Arg Tyr Cys Gly Met Leu Gly Thr
68 225                 230                 235                 240
70 Ala Thr Gly Gly Asn Leu Asp Cys Tyr Thr Gln Arg Asn Phe Ala Ser
71             245                 250                 255
73 <210> SEQ ID NO: 2
```

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/534,229A   TIME: 08:54:23

Input Set : A:\es.txt
Output Set: N:\CRF3\11142001\I534229A.raw

```
74  <211> LENGTH: 323
75  <212> TYPE: PRT
76  <213> ORGANISM: Triticum aestivum
78  <400> SEQUENCE: 2
80  Met Ser Thr Leu Arg Ala Arg Cys Ala Thr Ala Val Leu Ala Val Val
81  1               5                   10                  15
83  Leu Ala Ala Ala Ala Val Thr Pro Ala Thr Ala Glu Gln Cys Gly Ser
84                  20                  25                  30
86  Gln Ala Gly Gly Ala Lys Cys Ala Asp Cys Leu Cys Cys Ser Gln Phe
87              35                  40                  45
89  Gly Phe Cys Gly Thr Thr Ser Asp Tyr Cys Gly Pro Arg Cys Gln Ser
90      50                  55                  60
92  Gln Cys Thr Gly Cys Gly Gly Gly Gly Gly Val Ala Ser Ile Val
93  65                  70                  75                  80
95  Ser Arg Asp Leu Phe Glu Arg Phe Leu Leu His Arg Asn Asp Ala Ala
96                  85                  90                  95
98  Cys Leu Ala Arg Gly Phe Tyr Thr Tyr Asp Ala Phe Leu Ala Ala Ala
99                  100                 105                 110
101 Gly Ala Phe Pro Ala Phe Gly Thr Thr Gly Asp Leu Asp Thr Arg Lys
102             115                 120                 125
104 Arg Glu Val Ala Ala Phe Phe Gly Gln Thr Ser His Glu Thr Thr Gly
105     130                 135                 140
107 Gly Trp Pro Thr Ala Pro Asp Gly Pro Phe Ser Trp Gly Tyr Cys Phe
108 145                 150                 155                 160
110 Lys Gln Glu Gln Gly Ser Pro Pro Ser Tyr Cys Asp Gln Ser Ala Asp
111             165                 170                 175
113 Trp Pro Cys Ala Pro Gly Lys Gln Tyr Tyr Gly Arg Gly Pro Ile Gln
114             180                 185                 190
116 Leu Thr His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val
117             195                 200                 205
119 Asp Leu Leu Asn Asn Pro Asp Leu Val Ala Thr Asp Pro Thr Val Ala
120     210                 215                 220
122 Phe Lys Thr Ala Ile Trp Phe Trp Met Thr Thr Gln Ser Asn Lys Pro
123 225                 230                 235                 240
125 Ser Cys His Asp Val Ile Thr Gly Leu Trp Thr Pro Thr Ala Arg Asp
126             245                 250                 255
128 Ser Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn Val Ile
129             260                 265                 270
131 Asn Gly Gly Ile Glu Cys Gly Met Gly Gln Asn Asp Lys Val Ala Asp
132             275                 280                 285
134 Arg Ile Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Phe Gly Ile Gly Tyr
135     290                 295                 300
137 Gly Asn Asn Leu Asp Cys Tyr Asn Gln Leu Ser Phe Asn Val Gly Leu
138 305                 310                 315                 320
140 Ala Ala Gln
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 319
145 <212> TYPE: PRT
146 <213> ORGANISM: Triticum aestivum
```

```
148 <400> SEQUENCE: 3
150 Met Arg Gly Val Val Val Val Ala Met Leu Ala Ala Ala Phe Ala Val
151 1               5                 10                15
153 Ser Ala His Ala Glu Gln Cys Gly Ser Gln Ala Gly Gly Ala Thr Cys
154             20                  25                30
156 Pro Asn Cys Leu Cys Cys Ser Lys Phe Gly Phe Cys Gly Thr Thr Ser
157         35                  40                45
159 Asp Tyr Cys Gly Thr Gly Cys Gln Ser Gln Cys Asn Gly Cys Ser Gly
160     50                  55                60
162 Gly Thr Pro Val Pro Val Pro Thr Pro Ser Gly Gly Gly Val Ser Ser
163 65                  70                75                80
165 Ile Ile Ser Gln Ser Leu Phe Asp Gln Met Leu Leu His Arg Asn Asp
166             85                  90                95
168 Ala Ala Cys Leu Ala Lys Gly Phe Tyr Asn Tyr Gly Ala Phe Val Ala
169         100                 105               110
171 Ala Ala Asn Ser Phe Ser Gly Phe Ala Thr Thr Gly Ser Thr Asp Val
172         115                 120               125
174 Lys Lys Arg Glu Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr
175     130                 135               140
177 Thr Gly Gly Trp Pro Thr Ala Pro Asp Gly Pro Tyr Ser Trp Gly Tyr
178 145                 150               155               160
180 Cys Phe Asn Gln Glu Arg Gly Ala Thr Ser Asp Tyr Cys Thr Pro Ser
181             165                 170               175
183 Ser Gln Trp Pro Cys Ala Pro Gly Lys Lys Tyr Phe Gly Arg Gly Pro
184         180                 185               190
186 Ile Gln Ile Ser His Asn Tyr Asn Tyr Gly Pro Ala Gly Gln Ala Ile
187         195                 200               205
189 Gly Thr Asp Leu Leu Asn Asn Pro Asp Leu Val Ala Ser Asp Ala Thr
190     210                 215               220
192 Val Ser Phe Lys Thr Ala Leu Trp Phe Trp Met Thr Pro Gln Ser Pro
193 225                 230               235               240
195 Lys Pro Ser Ser His Asp Val Ile Thr Gly Arg Trp Ser Pro Ser Gly
196             245                 250               255
198 Ala Asp Gln Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn
199         260                 265               270
201 Ile Ile Asn Gly Gly Leu Glu Cys Gly Arg Gly Gln Asp Gly Arg Val
202         275                 280               285
204 Ala Asp Arg Ile Gly Phe Tyr Lys Arg Tyr Cys Asp Leu Leu Gly Val
205     290                 295               300
207 Ser Tyr Gly Asp Asn Leu Asp Cys Tyr Asn Gln Arg Pro Phe Ala
208 305                 310               315
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 23
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial/Unknown
215 <220> FEATURE:
216 <221> NAME/KEY: misc_feature
217 <222> LOCATION: (1)..(23)
218 <223> OTHER INFORMATION: Artificial primer.
```

C--> 213 <213> ORGANISM: Artificial/Unknown

(handwritten annotation:) 1. Invalid 213 response: Appropriate responses must be either "Artificial" or "Unknown" but not both.

(handwritten annotation:) 2. Either response requires an explanation in field 223.

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/534,229A   TIME: 08:54:23

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11142001\I534229A.raw**

```
        221 <400> SEQUENCE: 4
W-->    222 cacgagacca cnggcggntg ggc                                      23
        225 <210> SEQ ID NO: 5
        226 <211> LENGTH: 20
        227 <212> TYPE: DNA
C-->    228 <213> ORGANISM: Artificial/Unknown
        230 <220> FEATURE:
        231 <221> NAME/KEY: misc_feature
        232 <222> LOCATION: (1)..(20)
        233 <223> OTHER INFORMATION: Artificial primer.
        236 <400> SEQUENCE: 5
W-->    237 acnaatatca tcaacggcgg                                          20
        240 <210> SEQ ID NO: 6
        241 <211> LENGTH: 771
        242 <212> TYPE: DNA
        243 <213> ORGANISM: Triticum aestivum
        245 <220> FEATURE:
        246 <221> NAME/KEY: misc_feature
        247 <222> LOCATION: (1)..(771)
        248 <223> OTHER INFORMATION: cDNA
        251 <400> SEQUENCE: 6
        252 atggcgaggt ttgctgccct cgccgtgtgc gccgccgcgc tcctgctcgc cgtggcggcg   60
        254 gggggtgccg cggcgcaggg cgtgggctcg gtcatcacgc ggtcggtgta cgcgagcact  120
        256 ctgcccaacc gcgacaactc gctgtgcccg gccagagggt tctacacgta cgacgccttc  180
        258 atcgccgccg ccaacacctt cccgggcttc ggcaccaccg gcagcgccga cgacatcaag  240
        260 cgcgacctcg ccgccttctt cggccagacc tcccacgaga ccaccggagg gacgagaggc  300
        262 gctgccgacc agttccagtg gggctactgc ttcaaggaag agataagcaa ggccacgtcc  360
        264 ccaccatact atggacgggg acccatccaa ttgacagggc ggtccaacta cgatcttgcc  420
        266 gggagagcga tcgggaagga cctggtgagc aacccagacc tagtgtccac ggacgcggtg  480
        268 gtgtccttca ggacggccat gtggttctgg atgacggcgc agggaaacaa gccgtcgtgc  540
        270 cacaacgtcg ccctacgccg ctggacgccg acggccgccg acaccgctgc cggcagggta  600
        272 cccggatacg gagtgatcac caatatcatc aacggcgggc tcgagtgcgg aatgggccgg  660
        274 aacgacgcca acgtcgaccg catcggctac tacacgcgct actgcggcat gctcggcacg  720
        276 gccaccggag gcaacctcga ctgctacacc cagaggaact tcgctagcta g            771
        279 <210> SEQ ID NO: 7
        280 <211> LENGTH: 972
        281 <212> TYPE: DNA
        282 <213> ORGANISM: Triticum aestivum
        284 <220> FEATURE:
        285 <221> NAME/KEY: misc_feature
        286 <222> LOCATION: (1)..(972)
        287 <223> OTHER INFORMATION: cDNA
        290 <400> SEQUENCE: 7
        291 atgtccacgc tgagagcgcg gtgtgcgacg gccgtcctgg ccgtcgtcct ggcggcggcc   60
        293 gcggtcacgc cggccacggc cgagcagtgc ggctcgcaag ccggcggcgc caagtgcgcc  120
        295 gactgcctgt gctgcagcca gttcgggttc tgcggcacca cctccgacta ctgcggcccc  180
        297 cgctgccaga gccagtgcac tggctgcggt ggcggcggcg gcggggtggc ctccatcgtg  240
        299 tccagggacc tcttcgagcg gttcctgctc catcgcaacg acgcagcgtg cctggcccgc  300
        301 gggttctaca cgtacgacgc cttcttggcc gccgccggcg cgttcccggc cttcggcacc  360
```

```
303 accggagacc tggacacgcg gaagcgggag gtggcggcct tcttcggcca gacctctcac   420
305 gagaccaccg gcgggtggcc caccgcgccc gacggcccct tctcatgggg ctactgcttc   480
307 aagcaggagc agggctcgcc gccgagctac tgcgaccaga gcgccgactg gccgtgcgca   540
309 cccggcaagc agtactatgg ccgcggcccc atccagctca cccacaacta caactacgga   600
311 ccggcgggcc gcgcaatcgg ggtggacctg ctgaacaatc cggacctggt ggccacggac   660
313 ccgacagtgg cgttcaagac ggcgatatgg ttctggatga cgacgcagtc caacaagccg   720
315 tcgtgccatg acgtgatcac ggggctgtgg actccgacgg ccaggatag cgcagccgga    780
317 cgggtacccg ggtatggtgt catcaccaac gtcatcaacg gcgggatcca atgcggcatg   840
319 gggcagaacg acaaggtggc ggatcggatc gggttctaca agcgctattg tgacattttc   900
321 ggcatcggct acgggaataa cctcgactgc tacaaccaat tgtcgttcaa cgttgggctc   960
323 gcggcacagt ga                                                      972
```

326 <210> SEQ ID NO: 8
327 <211> LENGTH: 960
328 <212> TYPE: DNA
329 <213> ORGANISM: Triticum aestivum
331 <220> FEATURE:
332 <221> NAME/KEY: misc_feature
333 <222> LOCATION: (1)..(960)
334 <223> OTHER INFORMATION: cDNA
337 <400> SEQUENCE: 8

```
338 atgagaggag ttgtggtggt ggccatgctg ccgcggcct tcgccgtgtc tgcgcacgcc    60
340 gagcaatgcg gctcgcaggc cggcggggcg acgtgcccca actgcctctg ctgcagcaag   120
342 ttcggtttct gcggcaccac ctccgactac tgcggcaccg gctgccagag ccagtgcaat   180
344 ggctgcagcg gcggcacccc ggtaccggta ccgacccct ccggcggcgg cgtctcctcc    240
346 attatctcgc agtcgctctt cgaccagatg ctgctgcacc gcaacgacgc ggcgtgcctg   300
348 gccaaggggt tctacaacta cggcgccttc gtcgccgccg ccaactcgtt ctcgggcttc   360
350 gcgaccacag gtagcaccga cgtcaagaag cgcgaggtgg ccgcgttcct cgctcagact   420
352 tcccacgaga cgaccggcgg gtggccgacg gcgcccgacg gccctactc ctggggctac    480
354 tgcttcaacc aggagcgcgg cgccacctcc gactactgca cgccgagctc gcagtggcca   540
356 tgtgcgccgg gcaagaagta cttcgggcgc gggcccatcc agatctcaca caactacaac   600
358 tacggccgg cggggcaggc catcggcacc gacctgctca caacccgga ccttgtggcg     660
360 tcggacgcga ccgtgtcgtt taagacggcg ttgtggttct ggatgacgcc gcaatcaccc   720
362 aagccttcga gccacgacgt gatcacgggc cggtggagcc cctcgggcgc cgaccaggcg   780
364 gcggggaggg tgcctgggta cggtgtgatc accaacatca tcaacggtgg gctcgagtgc   840
366 gggcgcgggc aggacggccg tgtcgccgac cggatcgggt tctacaagcg ctactgcgac   900
368 ctccttggcg tcagctacgg tgacaacctg gactgctaca accaaaggcc gttcgcatag   960
```

VERIFICATION SUMMARY   DATE: 11/14/2001
PATENT APPLICATION: **US/09/534,229A**   TIME: 08:54:24

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11142001\I534229A.raw**

L:213 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:228 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5